Appl. No. 09/840,743
Amdt. dated June 10, 2003
Reply to Office Action of December 26, 2002

PATENT

Amendments to the Specification:

Please replace the title of the application on page 1 with the following rewritten title:

-- *DEMETER* NUCLEIC ACIDS ~~THAT CONTROL PLANT DEVELOPMENT~~ --

Please replace the paragraph beginning at page 17, line 19, with the following rewritten paragraph:

-- Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al, supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.--

Please replace the paragraph beginning on line 20 of page 43 with the following rewritten paragraph:

-- ~~The first consensus sequence listed above corresponds to amino acid positions 586 through 937 of SEQ ID NO:2. The second consensus sequence listed above corresponds to amino acid positions 1117 through 1722 of SEQ ID NO:2.~~ The consensus sequence provides amino acid

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sequences by position using single letter amino acid abbreviations. Numbers in carrots ("<" or ">") refer to amino acid positions where there is no consensus and which therefore, can be any amino acid. Amino acid abbreviations in parentheses indicate alternative amino acids at the same position. Capitalized letters refer to predominant consensus amino acids and lower case letters refer to amino acids that are commonly found in DMT sequences, but are not predominant.--

Please replace the abstract of the application on page 105 with the following rewritten abstract:

-- *DEMETER* NUCLEIC ACIDS ~~THAT CONTROL PLANT DEVELOPMENT~~

This invention is directed to plant genetic engineering. In particular, it relates to *DEMETER (DMT)* nucleic acids and polypeptides that control, for example, ~~modulating~~ seed (and in particular endosperm, embryo and seed coat) development, flowering time, chromosomal DNA methylation and ~~modulating~~ transcription in plants.--